

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 17:05:22 ; Search time 14 Seconds
(without alignments)
2130.106 Million cell updates/sec

Title: US-09-831-656-2

Perfect score: 3821

Sequence: 1 MKKRLSLFVGLMLLGLLF.....NHVATTPGTGNTVTWQN 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3713	97.2	717	1 AMYM_BACST	P19531 bacillus st
2	1737	45.5	718	1 CDGT_BACCI	P30920 bacillus ci
3	1729	45.2	718	1 CDGT_BACSS	P31747 bacillus sp
4	1721	45.0	710	1 CDGT_THETU	P26827 thermoanaer
5	1688.5	44.2	718	1 CDGT_BACLI	P14014 bacillus li
6	1669.5	43.7	713	1 CDG2_PAEMA	P31835 paenibacill
7	1623	42.5	714	1 CDG1_PAEMA	P04830 paenibacill
8	1588.5	41.6	713	1 CDGT_BACSP	P30921 bacillus sp
9	1585.5	41.5	713	1 CDGT_BACCI	P43379 bacillus ci
10	1574.5	41.2	711	1 CDGU_BACCI	P17977 bacillus st
11	1566.5	41.0	713	1 CDGT_BACST	P17692 bacillus st
12	1536.5	40.2	713	1 AMYR_BACS8	P05618 bacillus sp
13	1507	39.4	712	1 CDGT_BACS3	P09121 bacillus sp
14	1498.5	39.2	704	1 CDGT_BACOH	P27036 bacillus oh
15	1480.5	38.7	703	1 CDGT_BACS2	P31746 bacillus sp
16	1160	30.4	528	1 AMY_BACCI	P08137 bacillus ci
17	966.5	25.3	655	1 CDGT_KLEPN	P08704 klebsiella
18	634.5	16.6	1196	1 AMYB_PAEPO	P21543 paenibacill
19	480	12.6	494	1 AMY1_SACFI	P16950 saccharomyc
20	479.5	12.5	1475	1 APU_THETY	P16950 t amylopull
21	477.5	12.5	919	1 APU_STELI	Q05884 streptomyc
22	460	12.0	1481	1 APU_THET	P38939 t amylopull
23	453	11.9	512	1 AMY1_DEBOC	P19269 debaryomyc
24	451.5	11.8	1861	1 APU_THETU	P38536 t amylopull
25	450	11.8	499	1 AMYA_ASPO	P10529 aspergillus
26	448	11.7	499	1 AMY_ASPSH	P30292 aspergillus
27	444	11.6	498	1 AMYA_ASFAW	Q02905 aspergillus
28	444	11.6	499	1 AMYB_ASFAW	Q02906 aspergillus
29	439.5	11.5	478	1 YDDI_SCHPO	Q10427 schizosacch
30	432	11.3	484	1 AMYA_ASFNG	P56271 aspergillus
31	429	11.2	1279	1 APU_THESA	P36905 t amylopull
32	419	11.0	581	1 AMY1_SCHPO	Q09840 schizosacch
33	390	10.2	585	1 NEPU_THEVU	Q08751 thermoactin

34	388	10.2	569	1	AMY_STRVL	P22998 streptomyc
35	370.5	9.7	574	1	CDAS_THET	P29964 thermoanaer
36	365	9.6	588	1	NEPU_BACST	P38940 bacillus st
37	359.5	9.4	556	1	AMY_STRLM	P09794 streptomyc
38	354.5	9.3	676	1	AMY1_ECOLI	P25718 escherichia
39	353.5	9.3	586	1	AMY_STRGR	P30270 streptomyc
40	334.5	8.8	548	1	AMY4_PSEST	P32818 bacillus ac
41	334.5	8.8	586	1	AMYM_BACAD	P32070 pseudomonas
42	330	8.6	562	1	AMY2_DICTH	P14898 dictyoglomu
43	326	8.5	605	1	MAL2_ECOLI	P21517 escherichia
44	319.5	8.4	605	1	AMY_THECU	P29750 thermomonos
45	317	8.3	513	1	AMY3_SCHPO	O14154 schizosacch

ALIGNMENTS

RESULT 1						
AMYM_BACST						
ID	AMYM_BACST	STANDARD;	PRT;	717 AA.		
AC	P19531;					
DT	01-FEB-1991 (Rel. 17, Created)					
DT	01-FEB-1991 (Rel. 17, Last sequence update)					
DT	15-JUN-2002 (Rel. 41, Last annotation update)					
DE	Maltogenic alpha-amylase precursor (EC 3.2.1.133) (Glucan 1,4-alpha-maltohydrolase).					
GN	AMYM.					
OS	Bacillus stearothermophilus.					
OC	Bacteria; Firmicutes; Bacilliales; Geobacillus.					
OX	NCBI_TaxID=1422;					
RN	[1]					
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 34-45.					
RC	STRAIN=C599;					
RA	Diderichsen B., Christiansen L.;					
RT	"Cloning of a maltogenic alpha-amylase from Bacillus stearothermophilus."					
RL	FEMS Microbiol. Lett. 56:53-60(1988).					
CC	FUNCTION: CONVERTS STARCH INTO MALTOSE.					
CC	CATALYTIC ACTIVITY: Hydrolysis of (1->4)-alpha-D-glucosidic linkages in polysaccharides so as to remove successive alpha-maltose residues from the non-reducing ends of the chains.					
CC	SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.					
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CC	EMBL; M36539; AAA22233.1; -					
DR	PIR; S28784; S28784.					
DR	HSSP; P30920; 1CGT.					
DR	InterPro; IPR000461; Alpha_amylase.					
DR	InterPro; IPR002044; CBD_4.					
DR	InterPro; IPR002909; IPT_TIG.					
DR	Pfam; PF00128; alpha-amylase; 1.					
DR	Pfam; PF00686; CBM_20; 1.					
DR	Pfam; PF01833; TIG; 1.					
DR	Pfam; PF02806; alpha-amylase_C; 1.					
DR	ProDom; PD001568; CBD_4; 1.					
DR	SMART; SM00429; IPT; 1.					
DR	HydroLase; Glycosidase; Carbohydrate metabolism; Signal.					
FT	SIGNAL 1 33					
FT	CHAIN 34 717					
SQ	SEQUENCE 717 AA; 78723 MW; 945DA8DB69BB2433 CRC64;					

Query Match 97.2%; Score 3713; DB 1; Length 717;
Best Local Similarity 98.1%; Pred. No. 2.5e-198;
Matches 708; Conservative 2; Mismatches 4; Indels 8; Gaps 5;

QY 1 MKKTLISLVGLMLLIGLFGSLPYNPNAEASSSASVKGDVYQIIIDRFYDGDITNN 60
 Db 1 MKKTLISLVGLMLLIGLFGSLPYNPNAEASSSASVKGDVYQIIIDRFYDGDITNN 60
 QY 61 NPAKSYGLDPTKSKWKMYGGDLGVROKLPYLKQLGVTTIWLSPVLDNLDLTLAGTDNT 120
 Db 61 NPAKSYGLDPTKSKWKMYGGDLGVROKLPYLKQLGVTTIWLSPVLDNLDLTLAGTDNT 120
 QY 121 GYHGYTRDPKQIEEHFGNNTTDLVNDHQHNGIKVIVDFVPHNSTPFKANDSTFAEGG 180
 Db 121 GYHGYTRDPKQIEEHFGNNTTDLVNDHQHNGIKVIVDFVPHNSTPFKANDSTFAEGG 180
 QY 181 ALXNNCTYMGNYFDDATKGFHNGDISNWDDEYEAQWKNFTDPAGSLADLSQENGTIA 240
 Db 181 ALXNNCTYMGNYFDDATKGFHNGDISNWDDEYEAQWKNFTDPAGSLADLSQENGTIA 240
 QY 241 QYLTDAAVOLVAHAGDGLRIDAVKHFNSGFSKSLADKLYOKKIDFLVGEWYGGDPGTANH 300
 Db 241 QYLTDAAVOLVAHAGDGLRIDAVKHFNSGFSKSLADKLYOKKIDFLVGEWYGGDPGTANH 300
 QY 301 LEKVRVANNNGVNLDFDLNTVIRNVFGTFTOTMYDLNNMNVNOTGNEYKYKENLITFDN 360
 Db 298 LEKVRVANNNGVNLDFDLNTVIRNVFGTFTOTMYDLNNMNVNOTGNEYKYKENLITFDN 357
 QY 361 HDMRSFLSVNS-NKANLHQ-ALAFILTSRGT-PSIYVGTQEQYVAGNDPYNRGMMPAFDT 417
 Db 358 HDMRSFLSVNSKANKHQLLSFSL--RGVRPPIYGTQEQYVAGNDPYNRGMMPAFDT 415
 QY 418 TTATAKEVSTLAGLRNNAIAOYGTTRWINNDVYIYERKFFNDVVLVAINRNTOSYS 477
 Db 416 TTATAKEVSTLAGLRNNAIAOYGTTRWINNDVYIYERKFFNDVVLVAINRNTOSYS 475
 QY 478 ISGLQALPNSGYADYLSGLLGGNGISVNSGVSASFTLAPGAVSWQVYTSASAPQIGSV 537
 Db 476 ISGLQALPNSGYADYLSGLLGGNGISVNSGVSASFTLAPGAVSWQVYTSASAPQIGSV 535
 QY 538 APNMGIPGNVYTIIDKGFGTGTGTGVTATVKSQTSNRLEEVYVPPNMAAGLTDVKVTA 597
 Db 536 APNMGIPGNVYTIIDKGFGTGTGTGVTATVKSQTSNRLEEVYVPPNMAAGLTDVKVTA 595
 QY 598 GGVSSNLYSYNLSGTQTSVFTVKSAPPTNLGDKYIYLTGNIPELGNMSTDSGAVNNAQ 657
 Db 596 GGVSSNLYSYNLSGTQTSVFTVKSAPPTNLGDKYIYLTGNIPELGNMSTDSGAVNNAQ 655
 QY 658 GPLLAPNYPDWFFYFVSVPAGTIQPFKIKRADGTIOWENSGNHVATPTGATGNITWTW 717
 Db 656 GPLLAPNYPDWFFYFVSVPAGTIQPFKIKRADGTIOWENSGNHVATPTGATGNITWTW 715
 QY 718 QN 719
 Db 716 QN 717

RESULT 2

CDGT_BACCI STANDARD; PRT; 718 AA.
 AC P30920;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
 OS (Cyclodextrin-glycosyltransferase) (CGTase).
 OS Bacillus circulans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8;
 RX MEDLINE=91103970; PubMed=1368573;
 RA Nitschke L., Heeger K., Bender H., Schulz G.E.;
 RT "Molecular cloning, nucleotide sequence and expression in Escherichia
 coli of the beta-cyclodextrin glycosyltransferase gene from Bacillus
 circulans strain no. 8.";

RL Appl. Microbiol. Biotechnol. 33:542-546(1990).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RC STRAIN=8;
 RX MEDLINE=91117298; PubMed=1826034;
 RA Klein C., Schulz G.E.;
 RT "Structure of cyclodextrin glycosyltransferase refined at 2.0-A
 resolution.";
 RL J. Mol. Biol. 217:737-750(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).
 RC STRAIN=8;
 RX MEDLINE=90064533; PubMed=2531228;
 RA Hofmann B.E., Bender H., Schulz G.E.;
 RT "Three-dimensional structure of cyclodextrin glycosyltransferase from
 Bacillus circulans at 3.4-A resolution.";
 RL J. Mol. Biol. 209:793-800(1989).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RC STRAIN=8;
 RX MEDLINE=98226626; PubMed=9558324;
 RA Schmidt A.K., Cottaz S., Driaguez H., Schulz G.E.;
 RT "Structure of cyclodextrin glycosyltransferase complexed with a
 derivative of its main product beta-cyclodextrin.";
 RL Biochemistry 37:5909-5915(1998).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RC STRAIN=8;
 RX MEDLINE=98409292; PubMed=9738912;
 RA Parsiegla G., Schmidt A.K., Schulz G.E.;
 RT "Substrate binding to a cyclodextrin glycosyltransferase and
 mutations increasing the gamma-cyclodextrin production.";
 RL Eur. J. Biochem. 255:710-717(1998).
 CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
 of a 1,4-alpha-D-glucosidic bond.
 CC -1- COFACTOR: BINDS TWO CALCIUM IONS.
 CC -1- SUBUNIT: MONOMER.
 CC -1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
 IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
 IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
 ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
 ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
 MALTOOLIGOSACCHARIDE PRODUCED.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; X68326; CAA48401.1;
 DR PIR; S23674; ALBSCG.
 DR PDB; 1CGT; 31-JAN-94.
 DR PDB; 1CGU; 31-JAN-94.
 DR PDB; 3CGT; 27-MAY-98.
 DR PDB; 4CGT; 12-AUG-98.
 DR PDB; 5CGT; 12-AUG-98.
 DR PDB; 6CGT; 14-OCT-98.
 DR PDB; 7CGT; 12-AUG-98.
 DR PDB; 8CGT; 14-OCT-98.
 DR PDB; 9CGT; 14-OCT-98.
 DR InterPro; IPR000461; Alpha_amylase.
 DR InterPro; IPR002044; CBD_4.
 DR InterPro; IPR002909; IPT_TIG.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR Pfam; PF00686; CBM_20; 1.
 DR Pfam; PF01833; TIG; 1.
 DR Pfam; PF02806; alpha-amylase_C; 1.
 DR ProDom; PD001568; CBD_4; 1.